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&lt;120&gt; Non-selective cation channel

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&lt;140&gt; 09/812,143

&lt;141&gt; 2001-03-19

&lt;150&gt; 100 13 296.0

&lt;151&gt; 2000-03-17

&lt;160&gt; 11

&lt;170&gt; PatentIn Ver. 2.1

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&lt;212&gt; DNA

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gtggtggtac ccctggataa cctagggaac cccaactgtg acggccacca gcagggctac 2580
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<210> 5  
 <211> 871  
 <212> PRT  
 <213> Homo sapiens

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<400> 5
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Glu Leu Pro Gly Asp Glu Ser Gly Thr Pro Gly Gly Glu Ala Phe Pro
      20              25              30

Leu Ser Ser Leu Ala Asn Leu Phe Glu Gly Glu Asp Gly Ser Leu Ser
      35              40              45

Pro Ser Pro Ala Asp Ala Ser Arg Pro Ala Gly Pro Gly Asp Gly Arg
      50              55              60

Pro Asn Leu Arg Met Lys Phe Gln Gly Ala Phe Arg Lys Gly Val Pro
      65              70              75              80

Asn Pro Ile Asp Leu Leu Glu Ser Thr Leu Tyr Glu Ser Ser Val Val
      85              90              95

Pro Gly Pro Lys Lys Ala Pro Met Asp Ser Leu Phe Asp Tyr Gly Thr
      100             105             110

Tyr Arg His His Ser Ser Asp Asn Lys Arg Trp Arg Lys Lys Ile Ile
      115             120             125

Glu Lys Gln Pro Gln Ser Pro Lys Ala Pro Ala Pro Gln Pro Pro Pro
      130             135             140

Ile Leu Lys Val Phe Asn Arg Pro Ile Leu Phe Asp Ile Val Ser Arg
      145             150             155             160

Gly Ser Thr Ala Asp Leu Asp Gly Leu Leu Pro Phe Leu Leu Thr His

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			165					170					175				
Lys	Lys	Arg	Leu 180	Thr	Asp	Glu	Glu	Phe 185	Arg	Glu	Pro	Ser	Thr	Gly	Lys		
Thr	Cys	Leu 195	Pro	Lys	Ala	Leu	Leu 200	Asn	Leu	Ser	Asn	Gly 205	Arg	Asn	Asp		
Thr	Ile 210	Pro	Val	Leu	Leu	Asp 215	Ile	Ala	Glu	Arg	Thr 220	Gly	Asn	Met	Arg		
Glu 225	Phe	Ile	Asn	Ser	Pro 230	Phe	Arg	Asp	Ile	Tyr 235	Tyr	Arg	Gly	Gln	Thr 240		
Ala	Leu	His	Ile	Ala 245	Ile	Glu	Arg	Arg	Cys 250	Lys	His	Tyr	Val	Glu 255	Leu		
Leu	Val	Ala	Gln 260	Gly	Ala	Asp	Val	His 265	Ala	Gln	Ala	Arg	Gly 270	Arg	Phe		
Phe	Gln	Pro 275	Lys	Asp	Glu	Gly	Gly 280	Tyr	Phe	Tyr	Phe	Gly 285	Glu	Leu	Pro		
Leu	Ser 290	Leu	Ala	Ala	Cys	Thr 295	Asn	Gln	Pro	His	Ile 300	Val	Asn	Tyr	Leu		
Thr 305	Glu	Asn	Pro	His 310	Lys	Lys	Ala	Asp	Met	Arg 315	Arg	Gln	Asp	Ser	Arg 320		
Gly	Asn	Thr	Val 325	Leu	His	Ala	Leu	Val	Ala 330	Ile	Ala	Asp	Asn	Thr 335	Arg		
Glu	Asn	Thr	Lys 340	Phe	Val	Thr	Lys	Met	Tyr 345	Asp	Leu	Leu	Leu 350	Leu	Lys		
Cys	Ala 355	Arg	Leu	Phe	Pro	Asp	Ser 360	Asn	Leu	Glu	Ala 365	Val	Leu	Asn	Asn		
Asp	Gly 370	Leu	Ser	Pro	Leu	Met 375	Met	Ala	Ala	Lys	Thr 380	Gly	Lys	Ile	Gly		
Ile 385	Phe	Gln	His	Ile	Ile 390	Arg	Arg	Glu	Val	Thr 395	Asp	Glu	Asp	Thr	Arg 400		
His	Leu	Ser	Arg 405	Lys	Phe	Lys	Asp	Trp	Ala 410	Tyr	Gly	Pro	Val	Tyr 415	Ser		
Ser	Leu	Tyr	Asp 420	Leu	Ser	Ser	Leu	Asp 425	Thr	Cys	Gly	Glu	Glu 430	Ala	Ser		
Val	Leu	Glu 435	Ile	Leu	Val	Tyr	Asn 440	Ser	Lys	Ile	Glu	Asn 445	Arg	His	Glu		
Met 450	Leu	Ala	Val	Glu	Pro	Ile 455	Asn	Glu	Leu	Leu	Arg 460	Asp	Lys	Trp	Arg		
Lys	Phe	Gly	Ala	Val	Ser	Phe	Tyr	Ile	Asn	Val	Val	Ser	Tyr	Leu	Cy		

465		470		475		480
Ala Met Val Ile Phe Thr Leu Thr Ala Tyr Tyr Gln Pro Leu Glu Gly						
		485		490		495
Thr Pro Pro Tyr Pro Tyr Arg Thr Thr Val Asp Tyr Leu Arg Leu Ala						
		500		505		510
Gly Glu Val Ile Thr Leu Phe Thr Gly Val Leu Phe Phe Phe Thr Asn						
		515		520		525
Ile Lys Asp Leu Phe Met Lys Lys Cys Pro Gly Val Asn Ser Leu Phe						
		530		535		540
Ile Asp Gly Ser Phe Gln Leu Leu Tyr Phe Ile Tyr Ser Val Leu Val						
		545		550		555
Ile Val Ser Ala Ala Leu Tyr Leu Ala Gly Ile Glu Ala Tyr Leu Ala						
		565		570		575
Val Met Val Phe Ala Leu Val Leu Gly Trp Met Asn Ala Leu Tyr Phe						
		580		585		590
Thr Arg Gly Leu Lys Leu Thr Gly Thr Tyr Ser Ile Met Ile Gln Lys						
		595		600		605
Ile Leu Phe Lys Asp Leu Phe Arg Phe Leu Leu Val Tyr Leu Leu Phe						
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Met Ile Gly Tyr Ala Ser Ala Leu Val Ser Leu Leu Asn Pro Cys Ala						
		625		630		635
Asn Met Lys Val Cys Asn Glu Asp Gln Thr Asn Cys Thr Val Pro Thr						
		645		650		655
Tyr Pro Ser Cys Arg Asp Ser Glu Thr Phe Ser Thr Phe Leu Leu Asp						
		660		665		670
Leu Phe Lys Leu Thr Ile Gly Met Gly Asp Leu Glu Met Leu Ser Ser						
		675		680		685
Thr Lys Tyr Pro Val Val Phe Ile Ile Leu Leu Val Thr Tyr Ile Ile						
		690		695		700
Leu Thr Phe Val Leu Leu Leu Asn Met Leu Ile Ala Leu Met Gly Glu						
		705		710		715
Thr Val Gly Gln Val Ser Lys Glu Ser Lys His Ile Trp Lys Leu Gln						
		725		730		735
Trp Ala Thr Thr Ile Leu Asp Ile Glu Arg Ser Phe Pro Val Phe Leu						
		740		745		750
Arg Lys Ala Phe Arg Ser Gly Glu Met Val Thr Val Gly Lys Ser Ser						
		755		760		765
Asp Gly Thr Pro Asp Arg Arg Trp Cys Phe Arg Val Asp Glu Val Asn						

770                      775                      780  
 Trp Ser His Trp Asn Gln Asn Leu Gly Ile Ile Asn Glu Asp Pro Gly  
 785                      790                      795                      800  
 Lys Asn Glu Thr Tyr Gln Tyr Tyr Gly Phe Ser His Thr Val Gly Arg  
                     805                      810                      815  
 Leu Arg Arg Asp Arg Trp Ser Ser Val Val Pro Arg Val Val Glu Leu  
                     820                      825                      830  
 Asn Lys Asn Ser Asn Pro Asp Glu Val Val Val Pro Leu Asp Ser Met  
                     835                      840                      845  
 Gly Asn Pro Arg Cys Asp Gly His Gln Gln Gly Tyr Pro Arg Lys Trp  
                     850                      855                      860  
 Arg Thr Glu Asp Ala Pro Leu  
 865                      870

<210> 6  
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 <212> PRT  
 <213> Mus musculus

<400> 6  
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Ala Pro Leu

<210> 7  
 <211> 16  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: primer

<400> 7  
 cgtctgcact gctcag 16

<210> 8  
 <211> 15  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 8  
 ccttcgctgg aatcc 15



<210> 9  
<211> 17  
<212> DNA  
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gaggagagag gaaaagc 17

<210> 10  
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<220>  
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<400> 10  
catgcgacaga tttggtgc 18

<210> 11  
<211> 18  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: primer

<400> 11  
cacgaggac tcatatag 18